

IN THE CLAIMS

Please cancel Claims 6-10 and 23 and amend Claim 3 as follows:

1. *(Canceled)*
2. *(Canceled)*
3. *(Currently amended)* A method in a computer system for ~~analyzing and~~ displaying data on gene expression in a molecular topography, comprising:
 - (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic comprising a sequence identifier;
 - (ii) a second value for a second polynucleotide-characteristic different from said first characteristic comprising a measure of size of the polynucleotide; and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
 - (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and
 - (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.
4. *(Canceled)*
5. *(Canceled)*
6. *(Canceled)*
7. *(Canceled)*
8. *(Canceled)*
9. *(Canceled)*
10. *(Canceled)*

11. *(Previously amended)* A method in a computer system for displaying differences in gene expression, comprising:

(1) for each of a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to a method in a computer system for analyzing and displaying data on gene expression in a molecular topography, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

- (i) a first value for a first polynucleotide characteristic,
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
- (iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position in a two co-ordinate display space, and from the third value a peak at that position; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

(2) for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate display space.

12. *(Previously amended)* A method in a computer system for displaying differences in gene expression, comprising:

(1) for each of a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to a method, comprising:

-5-

- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
- (i) a first value for a first polynucleotide characteristic;
 - (ii) a second value for a second polynucleotide-characteristic different from said first characteristic; and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
- (b) calculating for each polynucleotide from the first and second values a position in a two-co-ordinate display space, and from the third value calculating a peak at that position; and
- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression
- (2) for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;
- (3) for each position, generating a peak for display from the difference; and
- (4) displaying the respective difference peak at each of the positions in the two co-ordinate display space,
- wherein differences are displayed only if they meet or exceed a threshold value.

13. *(Previously amended)* A method in a computer system for comparing gene expression, comprising:

- (1) for each of a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to claim 11,
- (2) for each position in the two co-ordinate display space subtracting a first measure of quantity in the first profile from a second measure of quantity in the second profile to generate respective difference values;
- (3) calculating from the respective difference values a measure of difference of the two profiles.

14. (*Previously amended*) The method of claim 13, wherein the first profile is a standard reference profile and the second profile is a profile of a test sample.

15. (*Original*) The method of claim 14, wherein comparison of the test sample profile with the standard reference profile is diagnostic of a condition or disease.

16. (*Original*) The method of claim 15, wherein the first profile is a profile of a reference sample and the second profile is a profile of a test sample.

17. (*Original*) The method of claim 16, wherein comparison of the profile of the test sample with the profile of the reference sample is diagnostic of a condition or disease.

18. (*Original*) The method of claim 13 wherein the difference value is set to zero when the difference between the first measure and the second measure is less than two-fold.

19. (*Original*) The method of claim 13 wherein the first profile is identical to the second profile when all the respective first and second measures are identical.

20. (*Original*) The method of claim 13 wherein the first profile is similar to the second profile when the average difference between the respective first and second measures is less than a predefined amount.

21. (*Canceled*)

22. (*Canceled*)

23. (*Canceled*)

24. (*Canceled*)